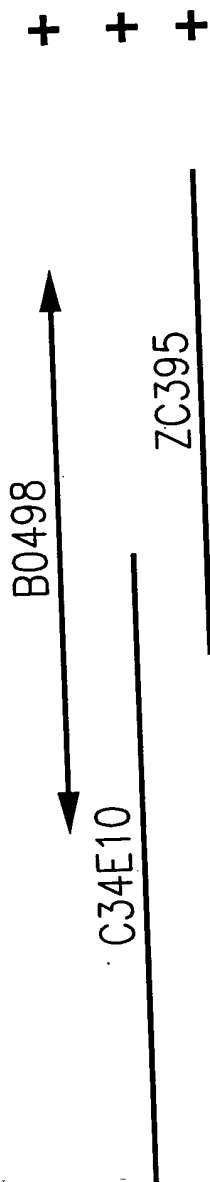


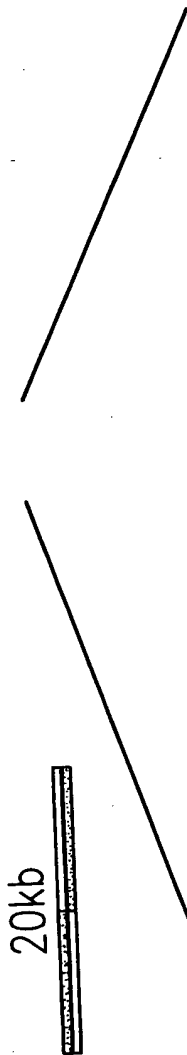


Rescue

711 - 2A



20kb

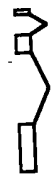


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Apal Ndel

spel



← ZC395.8  
2kb

pMQ2

pMQ3

pMQ4

5

$$+ \quad - \quad + \quad -$$

*gro-1*

SL2

M I F R K F L N F L K P Y K M R 16

aaaatatcgtcaggaaataataacatttcagatataccctgaactctacagtttATGATATTCAGGAAATTTCTGAATTTTCTGAAACCTTACAAAATGC 1394

T D P I I F V I G C T G T G K S D L G V A I A K K Y G G E V I S V 49

GAACGGATCCGATTATTTTCGTGATTGGGTGCACTGGAACCGGGAAAAGTGATCTTGGAGTGGCAATTGCAAGAAATATGGAGGAGAGGTGATTAGTGT 1494

SHP109

D S M Q F Y K G

L D I A T N K I T 66

AGATTC AATGCAATTTTATAAAGgtacatggggtttgtttcaattttaaattaattaattttcgtttttcagGACTTGACATTGCCACGAATAAGATAAC 1594

E E E S E G I Q H H M M S F L N P S E S S S Y N V H S F R E V T L 99

GGAAGAAGAATCTGAAGGGATTCAACATCATATGATGTCATTTTGAATCCATCTGAATCATCATCTTATAATGTACATAGTTCCGAGAAGTCACGTTG 1694

SHP94

D L I K

K I R A R S K I P V I V G 116

GATCTTATTAAGtgcttaattcgccactttttgaacttgatcctaattttcataattttcagAAAAATCCGCCCGTTCAAAAATTCCTGTAATTGTGCG 1794

SHP95

G T T Y Y A E S V L Y E N N L I E T N T S D D V D S K S R T S S E 149

GAGGAACCACTTATTATGCTGAAAGTGCCTTTATGAGAATAATCTGATTGAAACCAACACTTCAGATGACGTGGATTCCAAATCGAGAATCATCAGA 1894

SHP96

S S S E D T E E G I S N Q E L W D E L K K I D E K S A L L L H P N 182

ATCGTCATCTGAAGACACTGAAGAAGGAATTAGTAATCAAGAATTATGGGATGAATTGAAAAAATCGACGAAAAATCAGCACTTCTTCTACATCCAAAT 1994

FIS - 3A

*gro-1* continued...

4/32

N R Y R V Q R A L Q I F R E T G 198

AATCGTTATCGAGTACAGAGAGCATTGCAAATTTTCAGAGAACTGgtaattgatttgcaaattccagattaaaaacaaatcaagtaaagtttttgca 2094

I R K S E L V E K Q K S D E T V D L G G R L R F D N S L V I F M D 231

gGAATCCGAAAAAGTGAACCTGTTGAAAAACAGAAATCAGATGAACTGTTGATTGGGTGGACGACTACGATTGATAATCTTTAGTTATTTTATGG 2194

SHP97

A T P E V L E E R L D G R V D K M I K L G L K N E L I E F Y N E 263

ATGCAACACCTGAAGTTTGTAGAAGAAAGACTTGATGGAAGAGTTGATAAAATGATTAAATGGGTTTGAAGAATGAATTGATCGAGTTTATAACGAGgt 2294

aaatatttgaattttccagaaaaaaaagaaaatttttatttttggtttttttcttcttactattttccaaaaagtttaacttttgaaaac 2394

H A E Y 267

tgttcagaaaatgttcgtgtatttttttagcttactgaggcattatttcattgtgatttttactatactctataaaactaaattttcagCACGCCGAGTA 2494

I N H S K Y G V M Q C I G L K E F V P W L N L D P S E R D T L N G 300

CATAAATCACAGCAAATATGGTGTCAATGTATTGGTCTTAAAGAATTCGTTCCATGGCTCAATTTGACCCATCAGAAAGAGATACACTCAATGGG 2594

CG

e2400 lesion

SHP98

D K L F K Q G

C D D V K L H T R Q Y 318

GATAAATTGTTCAAGCAAGGgtaatttaaattttttcaatttttataaattccaagctattttcagATGCGATGATGTGAAGCTTCACACTCGACAAT 2694

FI 3B

*gro-1* continued...

5/32

A R R Q R R W Y R S R L L K R S D G D R

33

ATGCACGGCGCCAGAGACGGTGGTATCGATCGAGACTTTTAAACGGTCGGATGGTGATCGGgtatgttgattttaaaaaattgaatttttaagaact 279

▼ SHP99

ttttactaaattaacaaagtattggctgaaaatggctgaaaattatagtaaaactaatcaaaaaattgaaattttgaattaaagtcataaagtgcg 289

K M A S T K M L D 34

accagaaaattaaaaaaacatttttctattttaattaattcactctacttcactttaaaaataattttcagAAAAATGGCAAGTACAAAAATGCTGGAT 299

T S D K Y R I I S D G M D I V D Q W M N G I D L F E D 37

ACATCTGACAAGTACCGAATAATTAGTGATGGAATGGACATTCTTGATCAATGGATGAATGGAATCGATCTATTTGAAGATgtaaaatttcacaaattct 309

I S T D T N P I L K G S D A N I L L N C E I 39

aaaatttccgaatcacaaattaaaattttctacagATCTCCACAGACACCAATCCAATTCTAAAAGGGTCGGATGCAAATATTCTGCTGAATTGTGAAATC 319

C N I S M T G K D N W

Q K E I D G K K 41

TGTAATATTTCATGACTGGAAGATAATTGgtttgtttcaatacatattataatttcgaatgaatttttcagGCAGAAACATATCGATGGGAAAAA 329

SHP110 ▼

▼ SHP100

H K H H A K Q K K L A E T R T •

43

GCACAAGCATCATGCTAAGCAAAAGAAATTGGCAGAGACTCGCACataagacgctatattttttgttaacttaattttttgttgttgattgtt 339

polyA

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▼ SHP92

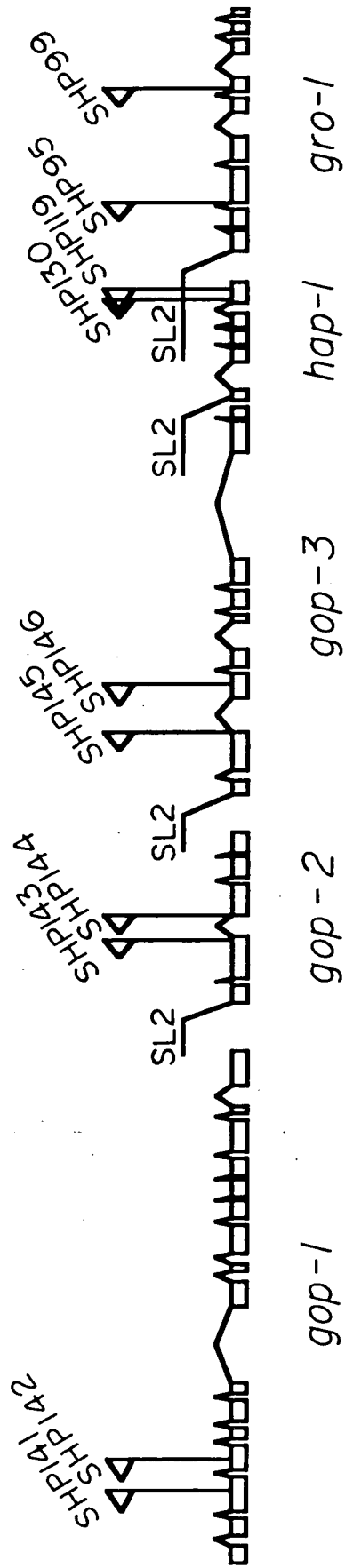
FISS 3C

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H A E Y I N H S K Y G V T 276

TTGGTCTTAAAGAATTCGTTCCATGGCTCAATTTGGACCCATCAGAAAGAGATACACTCAATGGGGATAAATTGT 1272  
L V L K N S F H G S I W T H Q K W I H S M G I N C 301

TCAAGCAAGGgtaatttaaattttttcaatttttataaattccaagctattttcagATGCCGATGATGtgaagcttc 1350  
S S K D A M H • 308

FIG. 30

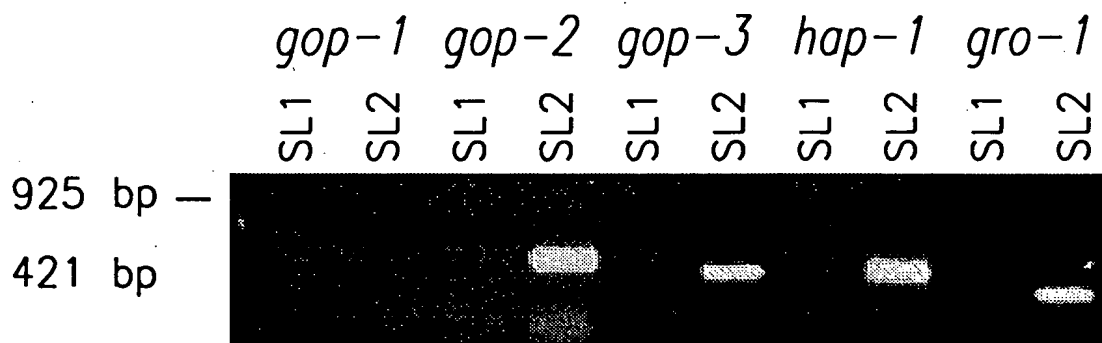


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FE-4A

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Fi 4B



# Sequence of GRO-1 and homologues

. . . . .

<i>C.elegans</i>	1	<u>M</u> IFRKFLNFLKPYK <u>M</u> RTDPIIFVIGCTGTGKSDLGVAIAKKYGGEVISVDSMQFYKGLDIATNKITEEESEGIQ
<i>S.cerevisiae</i>	1	<u>M</u> LKGPLKGCLN <u>M</u> SKKVIVIAGTTGVGKSQLSIQLAQKFNGEVINSDSMQVYKDIPITNKHPLQEREGIP
<i>E.coli</i>	1	MSDISKASLPKAIFLMGPTASGKTALAEIRKILPVELISVDSALIYKGM DIGTAKPNAEELLAAP

\_\_\_\_\_  
ATP/GTP  
binding site

. . . . .

<i>C.elegans</i>	76	HMMSFLNPSESSSYNVHSFREVTLDLIKKIRARSKIPVIVGGTTYAESVLYENNLIETNTSDDVDSKSRTSSE
<i>S.cerevisiae</i>	72	HVMNHVDWSE--EYYSHRFETECMNAIEDIHRRGKIPVIVGGTHYYLQTLFNKRVDTKSSERKLTRKQLDILES
<i>E.coli</i>	68	RLLDIRDPSQ--AYSAADFRRDALAEMADITAAGRIPLLVGGTMLYFKALLEGLSPLPSADPEVRARIEQQAEE

. . . . .

<i>C.elegans</i>	151	SSEDTEEGISNQELWDELKKIDEKSALLHPNNRYRVQRALQIFRETGIRKSELVEKQKSDETVDLGGRLRFDN
<i>S.cerevisiae</i>	147	DPDV-----IYNTLVKCDPDIAKYHPNDYRRVQRMLEIYYKTGKKPSETFNEQK-----ITLKFD-
<i>E.coli</i>	143	GWES-----LHRQLQEVDPVAAARIHPNDPQRLSRALEVFFISGKTLTTLTQTSG-----DALPYQV

FIG. 5A

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e2400

. . . . .

*C.elegans* 226 LVIFMDATPEVLEERLDGRVDKMIKLGKKNELIEFYNEHAEYINHSKYGVMQCIGLKEFVPWLNLDPSERDTLN  
*S.cerevisiae* 205 LFLWLYSKPEPLFQRLDDRVDMLERGAQEIKQLYEYYSQNKFTPEQCENGWQVIGFKEFLPWLTKGTDNT  
*E.coli* 202 QFAIAPASRELLHQRIEQRFHQMLASGFEAEVRALFARGDLHTDLP SIRC VGYRQMWSYLEGEISYDEM VYRGV

. . . . .

*C.elegans* 301 DKLFKQGCDDVKLHTRQYARRQRRWYRSRLLRSDGDRKMASTKMLDTS DKYRIISDGM DIVDQWMNGIDL FED  
*S.cerevisiae* 280 KLED CIERMKT--RTRQYAKRQVKWIKMLIPDIKGDILLDATDLSQWDTNASQRAIAISNDFISNRPIKQERA  
*E.coli* 277 -----ATRQLAKRQITWLRGWEGVHWLDSEKPEQARDEV LQVVGAIAG

.. . C2H2 zinc finger .

*C.elegans* 376 STDTNPILKGS DANILLNCEICNISMTGKDNWOKHIDGKKKHHAKQKKLATRT  
*S.cerevisiae* 353 KALEELLSKGETTMKKLDDWTHYTRNVCRNADGKNVVAIGEKYWKIHLGSRREKSNLKRNRTRQADFEKWKINKK

FiS - 5B

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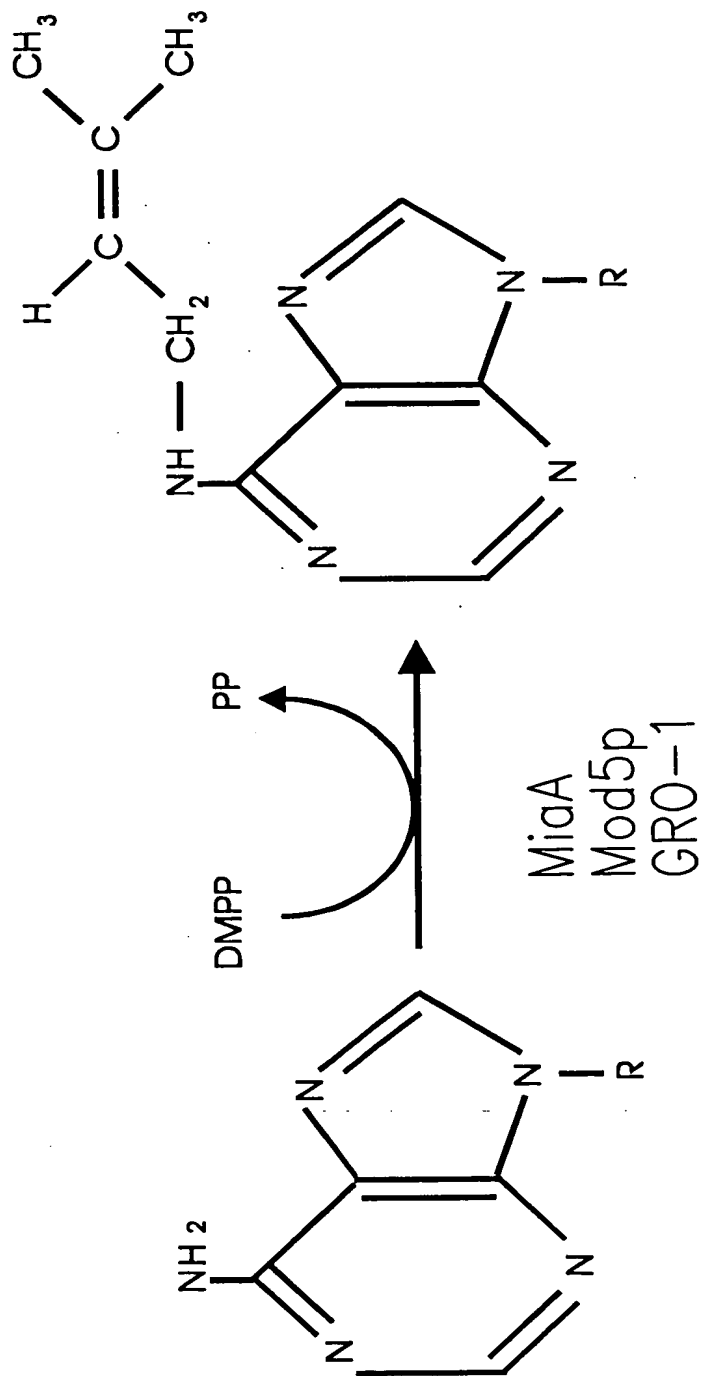


Fig. 6

# Sequence of HAP-1 and its homologues

... .

<i>H. sapiens</i>	MAASLVGKKIVFTGNAKKLEEVVQILGDKFP-----CTLVAQKIDLPEYXG-EPDEISIQKCQE
<i>C. elegans</i>	MLYILWKLNYLQKKMSLRKINFVTGNVKKLEEVKAILKNFE-----VSNVDVDLDEFQG-EPEFIAERKCRE
<i>S. cerevisiae</i>	MSNNEIVFVTGNANKLKEVQSILTQEVDNNNKTIHLINEALDLEELQDIDLNAIALAKGKQ
<i>E. coli</i>	MQKVVLATGNVGKVRSLASLSDFGLD-----IVAQTDLGVDSAEETGLTFIENAILKA

. . . . .

<i>H. sapiens</i>	AVRQV-QG-PVLVEDTCLCFNALGXLPGPYIKWFL--EKLKPEGLHQLLAGFED-----KSAYALCTFALSTGDP
<i>C. elegans</i>	AVEAV-KG-PVLVEDTSLCFNAMGGLPGPYIKWFL--KNLKPEGLHNMLAGFSD-----KTAYAQCIFAYTEG-L
<i>S. cerevisiae</i>	AVAALGKGPVVFVEDTALRFDEFNGLPGAYIKWFL--KSMGLEKIVKMLEPFEN-----KNAEAVTTICPADSRG
<i>E. coli</i>	RHAAKVLTALPAIADDSGLAVDVLGGAPGIYSARYSGEDATDQKNLQKLETMKDVDPDDQRARFHCVLVYLRAE

. . . . .

<i>H. sapiens</i>	SQPVRLFRGRTSGRIV-APRGQDFGWDPCFQP-DGYEQTYAEMPKAEKNAVSHRFRALLELOEYFGSLAA
<i>C. elegans</i>	GKPIHVFAKCPGQIV-APRGDTAFGWDPCFQP-DGFKETFGEMDKDVKNEISHRAKALELLKEYFQNN
<i>S. cerevisiae</i>	E--YHFFQGITRGKIV-PSRGPTTFGWDSEIFEPFDSHGLTYAEMSKDAKNAISHRGKAFQFKEYLYQNDF
<i>E. coli</i>	DPTPLVCHGSWPGVITREPAGTGGFGYDPIFFV-PSEGKTAELTREKSAISHRGQALKLLLDALRNG

mRNA sequence of human homologue of *gro-1*: hgro-1

CTGCCATAAG **ATG**GCGTCCG TGGCGGCTGC ACGAGCAGTT CCTGTGGGCA  
 GTGGGCTCAG GGGCCTGCAA CGGACCCTAC CTCTTGTAGT GATTCTCGGG  
 GCCACGGGCA CCGGCCAAATC CACGCTGGCG TTGCAGCTAG GCCAGCGGCT  
 CGGCGGTGAG ATCGTCAGCG CTGACTCCAT GCAGGTCTAT GAAGGCCTAG  
 ACATCATCAC CAACAAGGTT TCTGCCCAAG AGCAGAGAAT CTGCCGGCAC  
 CACATGATCA GCTTTGTGGA TCCTCTTGTG ACCAATTACA CAGTGGTGGG  
 CTTCAGAAAT AGAGCAACTG CTCTGATTGA AGATATATTT GCCCGAGACA  
 AAATTCCCTAT TGTTGTGGGA GGAACCAATT ATTACATTGA ATCTCTGCTC  
 TGGAAAGTTC TTGTCAATAC CAAGCCCCAG GAGATGGGCA CTGAGAAAGT  
 GATTGACCGA AAAGTGGAGC TTGAAAAGGA GGATGGTCTT GTACTTCACA  
 AACGCCTAAG CCAGGTGGAC CCAGAAATGG CTGCCAAGCT GCATCCACAT  
 GACAAACGCA AAGTGGCCAG GAGCTTGCAA GTTTTTGAAG AAACAGGAAT  
 CTCTCATAGT GAATTTCTCC ATCGTCAACA TACGGAAGAA GGTGGTGGTC  
 CCCTTGGAGG TCCTCTGAAG TTCTCTAACC CTTGCATCCT TTGGCTTCAT  
 GCTGACCAGG CAGTTCTAGA TGAGCGCTTG GATAAGAGGG TGGATGACAT  
 GCTTGCTGCT GGGCTCTTGG AGGAACTAAG AGATTTTCAC AGACGCTATA  
 ATCAGAAGAA TGTTCGGAA AATAGCCAGG ACTATCAACA TGGTATCTTC  
 CAATCAATTG GCTTCAAGGA ATTCACGAG TACCTGATCA CTGAGGGAAA  
 ATGCACACTG GAGACTAGTA ACCAGCTTCT AAAGAAAGGA CCTGGTCCCA  
 TTGTCCCCC TGTCTATGGC TTAGAGGTAT CTGATGTCTC GAAGTGGGAG  
 GAGTCTGTTC TTGAACCTGC TCTTGAAATC GTGCAAAGTT TCATCCAGGG  
 CCACAAGCCT ACAGCCACTC CAATAAAGAT GCCATACAAT GAAGCTGAGA  
 ACAAGAGAAG TTATCACCTG TGTGACCTCT GTGATCGAAT CATCATTTGGG  
 GATCGCGAAT GGGCAGCGCA CATAAAATCC AAATCCCCT TGAACCAACT  
 GAAGAAAAGA AGAAGATTGG ACTCAGATGC TGTCAACACC ATAGAAAGTC  
 AGAGTGTTTC CCCAGACTAT AACAAAGAAC CTAAAGGGAA GGGATCCCCA  
 GGGCAGAATG ATCAAGAGCT GAAATGCAGC GTTTAAGAGA CATGTCCAGT  
 GGCCTTTGGA AAGGTGGTGG GGATCCAGTT CAGGAGGGAG GGGTATGTTT  
 GTCTCCCAGT CTGGGCAAAG GAGTGCTATG CGGAATTCTC TGCATAGCAG  
 AAAAGCTCCC ACCATTTTCT TTTGATGTGG TTTTAAAGTC TCACGTTCTC  
 TATAATAGAA ACAGCAGGTC TTGTCAGCTC CTTGTGTGGC TGATGTGTCT  
 GGAAATGATG TAGTTCAGGA AAGCATTTTT TTTTCTTTG AACCTTAAAG  
 GTTCTATTAT TAAAAGCAGC ACAGATTCCA CATTTTATA CATGAGGATC  
 TTCTTTGTGG TGAATACCAG GATTGACTGC ATCCCTTTAA AAGAAGTTTT  
 ATGTCCCTGA CTCTGGCTAA AATTATCTAA TTTCCAGATG CTTTTGTAGA  
 TGA CTGAAGT ATTTGTGAGC CACATATTGG GAGTTCTAGA TTTGAGTGAA  
 TGGCAGGAAA GGGCCATCTC CATTGAGATG ATTAAGTGAA CCAAAC TAGT  
 TCTCGGAATT CTACAGAGAA GGAGGGAATC AGACTGAGGA AGCTGTGACA  
 TAGGACTTGA AGACCAAAGA CTTTGAAATT TGCAGCTGC TCATGTGTGA  
 GTTATTATCA CTGCTGTCTT TCTATTGAGT TACAAATCTA TATTTTATT  
 GAAGTTTAAA TAAAGAAAAA ATTTACAAGA AAAAAAAAAA A

# GRO-1 and its human homologue hgro-1p

hgro-1p      MASVAAARAVPVGSLRGLQRTLPLVVILGATGTGKSTLALQLGQRLGGEIVSADSMQVVEGLDIITN  
 GRO-1      MIFRKFLNFLKPYKMRTDPIIFVIGCTGTGKSDLGVAIAKKYGGEVISVDSMQFYKGLDIATN

hgro-1p      KVS AQEQRICRHHMISFVDPL-VTNYTVVDFRNRATALIEDIFARDKIPVVG GTNYYIESLLWKVLVN  
 GRO-1      KITEE ESEGIQHMMSF LNPSESSSYNVHSFREVTLDLIKKIRARSKIPVTVGGT TYAESVLYENNI

hgro-1p      TKPQEMGTEKVIDRKVELEKEDGLV-----LHKRLSQVDP EMAAKLHPHDKRKVARSLQVFEETGISH  
 GRO-1      ETINTSDDVD SKRTSSESSSEDT EEGISNQELWDELKKIDEKSALLHPNNRYRVQRALQIFRETGIRK

FI 9A

00 0 0 000 0 0 0 00 0000 000 0 00 00 0

SEFLHROHTEEGGGPLGGPLKFSNPCILWLHADQAVLDERLDKRVDDMLAAGLLEELRDFHRRYNQKNV

SELVEKOKSDETVD-LGGRLRFDNSLVIFMDATPEVLEERLDGRVDKMIKLGKKNELIEF---YNEHAE

0 0 0 0 0 0 0 . . 0 0

SENSODYOHGIFQSIGFKEFHEYLITEGKCTLETSNQLLKKGPGPIVPPVYGLE-----

YINHSKY--GVMQCIGLKEFVPLNLDPSERDTLNGDKLFGQGCDDVKLHTRQYARRQRRWYRSRLK

• • • • •

VSDVSKWEESVLEPALEIVQSFTQGHKPTATPIKMPYNEAENKRSYHL-----

RSDGDRKMASTKMLDTS DKYRIISDGMDIVDQWMNGIDLFE DISTDTNPILKGS DANILLN

● ● ● ● ● ● ●

CDLCDRITIGDREWAHIKSKSHLNQLKRRRLSDAVNTIESQSVSPDYNKEPKGKGSPGNDQELKCSV

CEICNISMTGKDNWQKHIDGKKHKHHAKQKKLAETRT

**C2H2 zinc finger**

FILE - 9B





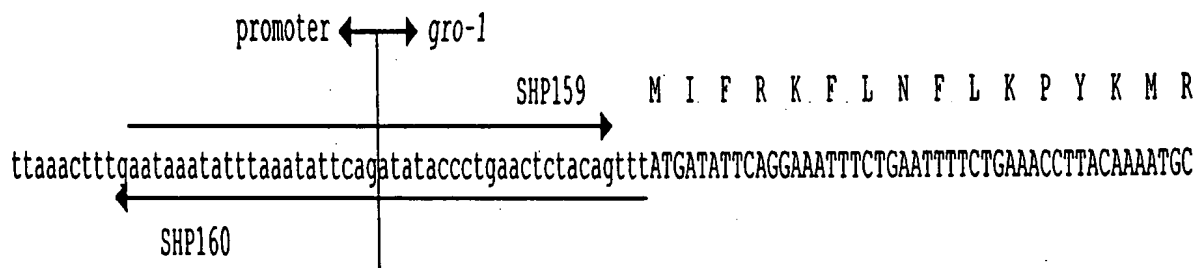
17/32

# Structure of pMQ8



gaaaattgagtcaaaaagttgagataaaacaaattaaacaattttctgaaaaataaacaactgaaatttgaagtaataaacaacacgcgaaaacgttat

ttcggagcatcgtttgagaagtaaaacttttttcggcgccaccttggtgcgcagttttatcttctctttaatttaattttcaagctaaatctttcttt



T D P I I F V I G C T G T G K S D L G V A I A K K Y G G E V I S V  
GAACGGATCCGATTATTTTCGTGATTGGGTGCACTGGAACCGGAAAAGTGATCTTGGAGTGGCAATTGCAAAGAAATATGGAGGAGAGGTGATTAGTGT

18/32

D S M Q F Y K G

L D I A T N . . .

AGATTCAATGCAATTTTATAAGgtacatgggttttgtttcaattttaattaattaatttcgtttttcagGACTTGACATTGCCACGAAT.....

. . . H A K Q K K L A E T R T .

.....CATGCTAAGCAAAAGAAATTGGCAGAGACTCGCACAtaagacgctatattttttgttaacttaattattttgttgttgattgtt

SHP170

[tctaga]tatact

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SHP162

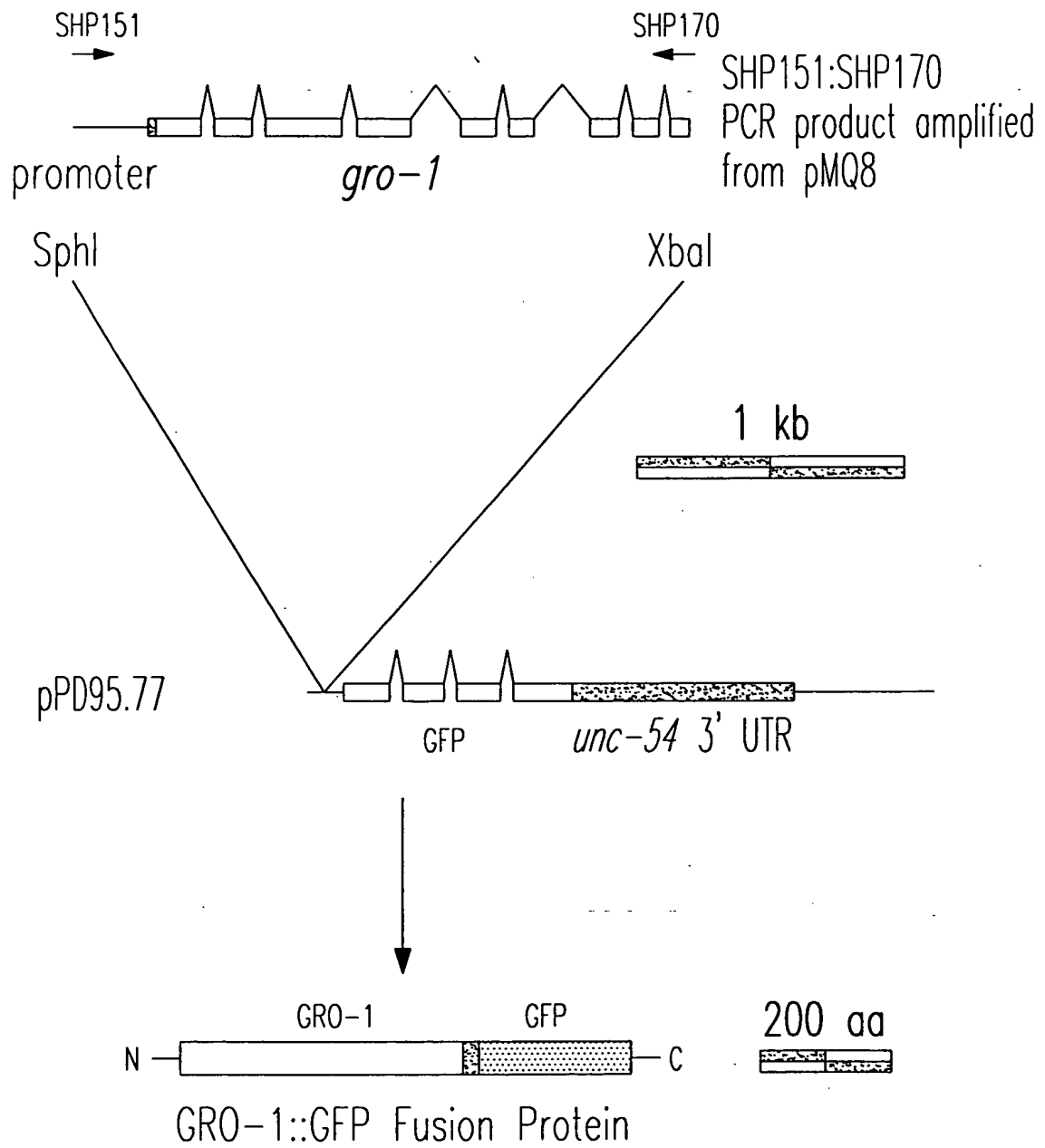
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PstI

FIG - 11B

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## Construction of pMQ18



20/32

*gop-1*

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aaaacaaattaaacaattttctgaaaaataaacaactgaaattgaagtaataaacaacacgcgaaaacgttatttcggagcatcgtttgagaagtaaa -9457

acttttttcggcgcacccttgtgcgcagttttatcttctcttttaatttaattttcaagctaaatctttcttttaactttgaataaatatttaaat -9357

M F R K L G S S G S L W K P K N P H S L E 21

attcagaatgcaccaataaacctggaacaaaatcgataATGTTCCGCAAGCTTGGTCTTCTGGGTCACATGGAAGCCGAAAAATCCGCATTCTTTGGA -9257

SHP190

Y L K Y L Q G V L T K N E K V T E N N K K I L V E A L R A I A E I 54

ATACCTCAAATATTACAAGGAGTGCTCACAAAAATGAGAAAGTTACGGAAAACAATAAGAAAATATTAGTAGAAGCATTACGAGCTATCGCAGAAATT -9157

L I W G D Q N D A S V F D F F L E R 72

CTCATTGGGGCGATCAGAATGATGCTTCGGTTTTTGAgtagagttttttccaatgtttttttcaaatctgatgttgaatttcagTTTCTTCCTTGAGC -9057

Q M L L Y F L K I M E Q G N T P L N V Q L L Q T L N I L F E N I R 105

GGCAAATGCTTCTTTATTCTTGAAAATTATGGAACAAGGAAACACACCCTAAATGTACAATTACTGCAGACTTTGAACATTTTATTCGAAAATATTGC -8957

SHP171

H E T S L Y F L L S N N H V N S I I 123

ACATGAAACTTCACTTTgtaagttttttatatggatttttcgcttaaaattgccagtttttcagATTTCCTTCTAAGTAACAATCATGTAAACTCGATTATT -8857

S H K F D L Q N D E I M A Y Y I S F L K T L S F K L N P A T I H F F 157

TCCCACAAATTCGATTACAAAATGATGAGATCATGGCTTACTACATTAGTTTCTGAAAACCTTTCATTAAACTGAATCCAGCTACAATCCACTTCT -8757

13A

*gop-1* continued...

21/32

F N E T T E E F P L L V E V L K L Y N W N E S M V R I A V R N I L 190  
TCTTCAATGAAACGACTGAAGAATTTCCATTGTTGGTAGAAGTTTTGAAGCTTTATAATTGGAATGAATCAATGGTTCGAATTGCTGTTAGAAATATTCT -8657

SHP141

SHP172

L N I V R V Q D D S M I I F A I K H T K 210  
TTTAAATATTGTGAGAGTTCAAGATGATTCAATGATTATTTTCGCTATCAAGCATACAAAgttagtagaaaattatthttgaaaagggtgatttaagcaa -8557

E Y L S E L I D S L V G L S L E M D T F V R S A E N V L A N 240  
taaattattacagGAATATCTATCGGAGTTAATAGATTCTCTAGTTGGTCTCTCACTTGAAATGGACACATTGTACGATCTGCTGAGAATGTGTTAGCTA -8457

R E R L R G K V D D L I D L I H Y I G E L L D V E A V A E S L S I 273  
ATCGAGAGAGATTACGAGGAAAAGTGGATGATTTAATTGATTGATTATATTGGTGAACATTGGATGTGAAGCTGTGCGCGAAAGTTTATCAAT -8357

SHP142

SHP173

L V T T R Y L S P L L L S S I S P R 291  
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R D N H S L L L T P I S A L F F F S E F L L 313  
GAAGAGATAATCATTCACTTCTACTCTCGATTCTGCGTTATTTTTTCTCTGAATTTTATTGgtgagttttaacattttaaattacatttttct -8157

I V R H H E T I Y T F L S S F L F D T Q N T L T T H W I 341  
aatttattttttcagATAGTTCGTCACCATGAACAATATATACATTTTTTATCATCTTTCCTATTGACACTCAGAATACTTTGACGACCCATTGGA -8057

R H N E K Y C L E P I T L S S P T G E Y V N E D H 366  
TACGTCATAATGAGAAATATTGCTTAGAACCGATTACATTATCATCAACCGGAGAATATGTGAATGAGACCAgtaagagctgaaatttttaaattt -7957

V F F D F L L E A F D S S Q A D D S K A F Y G L M 391  
ttgctttgaaatagtatthttcagCGTATTTTTCGATTTTCTACTGGAAGCATTTGATTCCAGTCAAGCAGACGATTCGAAGGCATTCTATGGATTAAATG -7857

FiS - 13B

*gop-1* continued...

L I Y S M F Q N N A

401

CTGATTTATTCAATGTTTCAGATAATGgtgagttttaaaaaattgatttgtaaattaaaattccatttccaataactcctcttcagacagtaagttt -7757

tcaatggtgtaaagttcctggtcatctgtgatcgttttcttcatttttttagtttgcatgaacagttttcaaatttttgatatcatagtaaatat -7657

cgtcatccagataattttctatttaaaaaaaatgaataaaaagagggcgcgagaaattgccgaagtaagttaaatttaagggacacatgcgtagcttg -7557

ttgtgtgggtctcgccgcgctttgtttgatttatctgttttctgctcaaagagctgtttttatttagcgttgatgctttttaccgttctcatcggc -7457

ttttaataggaatatttaaaaaaaagggttaataaatcttcgtttttacaaatccatctaagatttgcatgtggaagctcaacaagtaagtttta -7357

agtaacattgttttttaaaaaacaattgaaccaaattttgccgaaacattaataacatgacgatactctataaaatattcctcttttcaaaataaatttt -7257

D V G E L L S A A N F P V L K E S T T T S L A Q Q N 427

caaaaaaatccatttttcagCCGATGTTGGAGAACTTCTATCTGCTGCCAACTTCCCAGTGTCTCAAAGAATCAACGACAACCTTCATTAGCTCAACAGAA -7157

▼ SHP174

L A R L R I A S T S S I S K R T R A I T E I G V E A T E E D E I F 480

TCCTGCTCGTCTCCGAATAGCATCTACGTCTTCCATATCAAAGCGAACGAGAGCTATCACTGAAATTGGAGTAGAAGCGACCGAGGAAGATGAGATTTT -7057

▼ SHP185

H D V P E E Q T L

469

CATGATGTTCTGAAGAACAACGTTGgtaagtaataaatcaacattgattgttacacaaactttaatattttaaaatttgaaaattttcttcaaagt -6957

E D L V D D V L V D T E N S A I S D P E

489

ctcaaaaatcctgtcgaaaattacagGAAGATCTGGTGGATGATGATTGGTTGATACTGAAAATTGAGCAATAAGTGATCCAGAAgtgagtagaaaaacg -6857

P K N V E S E S R 498

tgcatgtattaattatttaaaaaaaatatagttttcccagttttccttgacctaaaactcagcaatttcagCCTAAAAACGTGGAGTCAGAACTCTCGT -6757

FI-13C

*gop-1* continued...

23/32

S R F Q S A V D E L P P P S T S G C D G R L F D A L S S I I K A V G 532  
TCTCGATTTCATCTGCTGTTGATGAGCTTCCACCTCCGTCGACTTCTGGATGTGATGGTCGACTTTTGTGACTTTCATCGATTATCAAAGCAGTTG -6657

T D D N R I R P I T L E L A C L V I R Q I L M T V D D E K 561  
GAACAGATGACAATCGAATTCGACCAATTACATTGGAACCTGCATGTCTTGTAAATTCGGCAAATTTTAATGACTGTTGATGATGAAAAgtaagattaca -6557

**SHP175**

V H T S L T K L C F E V R L K L L S 579  
aattcaaaattgagcaaaatcagaatctaaatttcataaattgttcagGTACATACCAGTTTAACGAAATTATGCTTCGAAGTTCGTCTAAACTTTTAT -6457

S I G Q Y V N G E N L F L E W F E D E Y A E F E 603  
CATCAATTGGACAATATGTTAATGGAGAGAATCTGTTTTGGAGTGGTTGAGGATGAATATGCAGAATTTGAAgtaagccaagaggtccgaaaataatt -6357

V N H V N F D I I G H E M L L P P A A T P L S N L L L 630  
taattcatcctttttattcagGTGAATCACGTGAATTTTCGATATAATCGGTCACGAAATGCTTCTCCTCCAGCTGCAACTCCTCTTCGAATCTGCTAC -6257

H K R L P S G F E E R I R T Q I V 647  
TTCATAAGCGATTGCCAGTGGATTTGAAGAACGAATAAGAACTgtaggaaactttttaaatttgaaaattaattatatatatattgcagCAAATCGTA -6157

F Y L H I R K L E R D L T G E G D T E L P V R V L N S D Q E P V A I 681  
TTCTACCTACATATTCGAAAATTGGAACGAGATTGACCGGTGAAGGAGACACAGAATTACCTGTGAGAGTGTGAATTCTGATCAGGAACCACTTGCCA -6057

G D C I N L H N S D L L S C T 696  
TCGGTGATTGTATTAATTACgtgagttcatctgcatagaaaacaccatatttctactcaaattaacaattttcagATAATTCGGATCTTCTATCCTGCA -5957

V V P Q Q L C S L G K P G D R L A R F L V T D R L Q L I L V E P D 729  
CTGTGGTTCCTCAACAACTATGTTCTCTTGGAAAACCTGGTGATCGTCTTGCTCGATTCTTGTCACTGATAGACTTCAATTAATTCITGCGAACCGGA -5857

**SHP176**

S R K A G W A I V R F V G L L Q D T T I N G D S T D S K V L H V V 762  
TTCTCGAAAAGCCGGATGGGCAATTGTTTCGATTCTAGGACTTCTTCAAGATACAACAATTAATGGAGATTCTACGGATTCGAAAGTTTTCATGTTGTG -5757

**SHP177**

V E G Q P S R I K K R H P V L T A 779  
GTGGAAGGGCAACCTCGAGAATTAAGgtaagaataactaacgggaaaaaaaatcaaaaattacttctgtttcagAAAAGACATCCGGTTTAACTGCA -5657

*gop-1* continued...

A F I F D D H I R C M A A K Q R L T K 798  
 AAGTTCATATTCGATGATCACATTCGGTGTATGGCAGCAAAGCAACGGCTCACCAAGgtaacggaataacccaaagacggaagtattgtaaat -5557

ggacgaaatcggcgaaattaattgaaaacgttgaatttgcgctaaaacaaacgaaacgaagcgaatttaactatcccttcaggtagaat -5457

G R Q T A R G L K L Q A I C S A L G V P R I D P A T 824  
 atacattttatttctctttatagGGTCGCCAACAGCAGCTGGTCTGAAACTTCAGGCGATATGTTGAGCTCTGGAGTCCACGTATCGATCCAGCGAC -5357

M T S S P R M N P F R I V K G C A P G S V R K T V S T S S S S S Q 857  
 AATGACGTCATCACCACGAATGAATCCATTCAGAATTGTGAAAGGATGCGCACCGGGAAGGTACGAAAACGTGTTCCACATCATCATCGTCAAGCCAA -5257

G R P G H Y S A N L R S A S R N A G M I P D D P T Q P S S S S E R R 891  
 GGACGTCCCGGACATTATTCTGCAAATCTTAGATCAGCATCTAGAAATGCAGGAATGATACCAGATGATCCAACTCAACCGAGTAGTTCTTCGGAAGAA -5157

**SHP178** ▼

S • 892  
 GATCCTagggatcaatatctcttcagtttcatctttatgctgtaaattgtatttaagtattcctattctttgtagtactgtatttacacatcgctctag -5057

ttaaaatcacaatctccgaaaaacaaaccagtgaacatgtgatatttctcttgcccatagttctcttttttttgaacaaaaacaattactttat -4957

gctcacctattcgagccatatTTTTTCCAATTaccggtgtttattttaatttctTTTTTTTTctgtaaatctactttattttaaaactgcatttg -4857

polyA  
 └─

agattgtgtatatTTTTTcaaatggttcaaatgccgaatctatctactt -4807



*gop-2*

25/32

SL2

M A E K A E N L P S S S A E A S E 1  
tttaatcattattcaaacagaaaaaccgattatttattcagattctcaaaaATGGCTGAAAAAGCTGAAAATCTCCATCTTCTTCGGCCGAGCTTCAG -470

E P S P Q T G P N V N Q K P S I L V L G M A G S G K T T F V Q 4  
AAGAGCCATCACCTCAAACGGACCAAATGTGAATCAAAAACCATCGATTTTGGTTCTTGAATGGCTGGTCTGGAAAAACGACATTGTTTCAGgtaac -460

R L T A F L H A R K T P P Y V I N L D P 6  
tttcattcaattttgagagttttcaacattactattttcagCGTCTCACAGCATTCCTACATGCTCGTAAACACCTCCATATGTGATTAATCTGGATC -450

A V S K V P Y P V N V D I R D T V K Y K E V M K E F G M G P N G A 10  
CGGCAGTTAGCAAAGTACCTTATCCAGTGAATGTTGACATTCGAGATACTGTGAAATACAAGGAAGTTATGAAAGAATTCGGAATGGGACCAAATGGAGC -440

▼  
SHP179

I M T C L N L M C T R F D K V I E L I N K R S S D F S V C L L D T 13  
AATTATGACATGTCTTAACCTGATGTGACTCGTTTGATAAAGTAATTGAGTTGATTAATAAGAGATCTTCTGATTTCTCAGTTTGTCTTCTTGATACT -430

▼  
SHP180

P G Q I E A F T W S A S G S I I T D S L A S S H P T 16  
CCTGGACAAATTGAAGCATTCATTGGAGTGCTAGTGGATCTATTACTGATTCATTGGCAAGTAGCCATCCCACGgtaagggttttgatttatgaa -420

▼  
SHP143

atctgcttgaaatgaaaaagattctaataaattttgacttttaaacattttttacagttatatttggtctattttctatcattaaaagcaaatgaaa -410

V V M Y I V D S A R A T N P T T F M S N 18  
agtcgattctactccatatttattaatttcgacttttcagGTGGTAATGTACATTGTGGATTCCGCTCGTGCCACAAATCCAACCTACATTCATGTCCAAT -400

▼  
SHP144

115 - 14A

*gop-2 continued...*

26/32

M L Y A C S I L Y R T K L P F I V V F N K A D I V K P T F A L K W M 21  
ATGCTCTACGCATGTTCCATTCTCTACCGTACCAAACCTCCATTTCATTGTCGTTTTCAACAAAGCTGATATTGTCAAACCAACATTTGCACTCAAATGGA -390

Q D F E R F D E A L E D A R S S Y M N D L S R S L S L V L D E F Y 24  
TGCAAGATTTCGAAAGATTGATGAAGCTTTAGAGGATGCCAGAAGCAGTTATATGAATGATTGAGTCGTTTCATTGAGTCTCGTTCTTGATGAATTCTA -380

SHP181

C G L K T V C V S S A T G E G F E D V 26  
TTGCGGACTGAAACAGgtttttatttcgaaataaaaccttttttaataataaatttcagTTTGGCTCAGTTCTGCAACTGGAGAAGGATTGCAAGATGT -370

M T A I D E S V E A Y K K E Y V P M Y E K V L A E K K L L D E E E 29  
AATGACAGCAATCGATGAAAGTGTGAAGCATACAAAAAGAATATGTTCCAATGTATGAAAAAGTGTGGCTGAGAAAAAACTATTGGATGAGGAGGAG -360

R K K R D E E T L K G K A V H D L N K V 31  
AGAAAGAAAAGAGATGAAGAGgtaattgtagtaatttaattctgattatcttcaaattttcagACTCTGAAAGGAAAAGCTGTTACGACCTGAACAAAG -350

A N P D E F L E S E L N S K I D R I H L G G V D E E N E E D A E L 35  
TCGCCAATCCCGACGAATTTCTGGAGTCGGAGTTGAATTCAAAAATCGATAGAATTCATTGGGCGGAGTCGATGAAGAGAATGAGGAGGATGCTGAAC -340

SHP182

E R S • 35

CGAAAGATCCTgattttctttttgtttttgaatttttattctattttgatccctgtttacttcttattgttctcattttgttgcgttgtttacatttta -330

polyA

ctcatttttgcataaacttggttgcaaaaatcaatataattttgatctggaaatggttttaaaccttaacctttcatatattaataatttttttcaaaa -320

aaacgttctaaaaagggttcctcattttttcaatataggaaattttgaaga -315

FiS - 14B

*gop-3*

27/32

SL2

M S E K T F H K 8

tcttttccaaaatgaggttcttcgcttgaaaagccaacatttaaaccctttttttccagaaacctagtggtaATGTCTGAAAAGACGTCCACAAG -3057

A Q T I R A K A S G V P S I V E A V Q F H G V R I T K N D A L V K E 42

GCACAGACCATCCGTGCAAAGGCATCCGGAGTGCCTTCAATCGTGAAGCTGTACAGTTTCATGGAGTTCGCATCACAAAAACGATGCTTTGGTTAAGG -2957

V S E L Y R 48

AGgtactacccaaatttcaaaatggtgcacaattcaattgaaaatataaattgtgaattaaattcaacttacatgttttttcagGTTCCGAATTATACA -285

S K N L D E L V H N S H L A A R H L Q E V G L M D N A V A L I D T 81

GAAGTAAAAATCTAGATGAACCTGTTTCATAACTCTCATCTGGCGGCTCGTCATCTTCAAGAAGTTGGATTAAATGGATAATGCAGTTGCTCTAATTGATAC -275

▼ SHP183

S P S S N E G Y V V N F L V R E P K S F T A G V K A G V S T N G D 114

ATCTCCAAGCTCAAATGAAGGATATGTTGTCAATTTCTAGTTCGAGAACCAAAATCATTCAGTCTGGAGTCAAAGCAGGAGTTTCAACGAATGGAGAT -26

A D V S L N A G K Q S V G G R G E A I N T Q Y T Y T V K 14

GCGGATGTCAGTTTAAATGCCGGAACAAAGTGTGGAGGACGAGGAGGCAATCAATACACAGTATACATATACTGTAAAGgtaaggacgagagttg -255

▼ SHP145

gcactgccagtttgcatgttctcccaatatttttaattataaaatttgaagtataaaaaatgtttgcttcactctaaaaatagccttttccatga -245

aaaaaattgaaaaaagtgtctaaaaatttcagaaatttccaatttccaacaatttggagaactttcaaaaattttccaactgaaattaaagctata -235

FI 15A

*gop-3* continued...

28/32

G D H C F 147

ttctatcactaaatattatacaagctctaagagaaaatgatgaagtggtcattttgtagaatttcctaaaaataatattcttcagGGCGATCACTGCTT -225

N I S A I K P F L G W Q K Y S N V S A T L Y R S L A H M P W N Q S 180

CAACATTTCCGCAATCAAACCATTCCTGGGATGGCAAAAATATTCGAATGTATCAGCGACTCTATACCGTTCACCTGCACATATGCCATGGAATCAATCA -215

SHP138

SHP146

D V D E N A A V L A Y N G Q L W N Q K L L H Q V K L N A 208

GATGTTGATGAGAATGCAGCTGTTCTTGCATATAATGGACAACATATGGAATCAAAAGCTTTTGCATCAAGTCAAATTGAATGCGgtaaagtattataagt -205

I W R T L R A T R D A A F S V R E Q A G H T L 23

gttttgccaaactatgatacagttcttcagATATGGAGAACACTTCGTGCCACTCGAGATGCCGCATTTTCAGTTCGTGAACAAGCCGGACACACTTTG -195

K F S L E N A V A V D T R D R P I L A S R G I L A 25

AAATTCCTCGTTGGAGAATGCTGTAGCTGTTGATACAAGAGATAGACCTATTCTTGCAAGTCGTGGAATTCCTGgtaaagtaacaacgactatttttaa -185

aaatatctttttcgaaaaattacgaacgaaaaaaactgtattatgtacccaacgcgaaattttgcagttcttgcgcgttcttgttgataaaaaatat -175

R F A Q 26

gtaaaaattggaaaaactacgaaaagtcgataaaaattccgtaccaaccggaaaatgtttcattaatttctcttcttttttcagCTCGTTTGTCTCAA -165

E Y A G V F G D A S F V K N T L D L Q 279

GAGTACGCAGGAGTATTGGTGATGCGTCATTTGTGAAGAATACATTAGATTTACAGgtacaaccttatttcaacaattatttcaaattctattaaaaa -155

SHP139

A A A P L P L G F I L A A S F Q A K H L K G L G D R E V H I L 31

taattccagGCAGCTGCCCCCTCTCCACTCGGTTTCATTCTTGCCGCCCTCATTCGAAGCGAAACATTTGAAAGGACTCGGAGATCGAGAAGTTCATATT -145

SHP140

*FE* 15B

*gop-3 continued...*

330

TGGATAGATGTTATTGGGTGGACAACAGGATGTCGAGGATTGGTCTGAATACTATTGGAgtgaqtlttaacgaaattctcttgaagtc aaataatc -1357

SHP184

361

atlttcagGTTAAAGCAGATAACAGTTGTCTTGGAGGAGGTGCTTCACCTGCTGGTGTGCTTCATTGTATCGGCCATTGATTCCACCAAAATATGCTATT -1257

394

TGCACAGCATTCCTTGCATCTGGAAGTGTGCATCAGTTCATTCCAAAATTTGGTGCACAATTACAGGATACTCAACGAGTATCAGCCGGATTGgt -1157

**SHP163**

gaqtttgaatttaqgaacatttggatgaaatgtatttttaaaatagatcagctttattttatttgaaaaaaacgctcattaatcaatagtgtatgt -1057

tccattctgaattttcttcttctctcgcggaatacaattttgaacttgttcgcacaccttctgtgtactttgtcaccaatcttctcatcaactaaatct -957

cgaaactgaaaaaatttcaaaattattccaaaaaatattgatgcagactacctttttgatggcttctggtacgtttctagcgtcgaatggattggctcct -857

ccaataattaaagtctcgttcggtagtttagccagacggacggtgtgcttcaacatTTTTCTAATTAATCTATTTCAATTCAAGTCACTCACTCTCTCT -757

*gop-3* continued...

gacgtcttctctatattccaagaactctgcagaaaatccgtgtccgccttgtgtgttctagtggcgtcggaggattcacgggtccaagacgaatgga -657

tgtctaaaaaatgttatattttgcataaagaaaacaccataccttcaccactttttgagttgtggcgcttctgaatggaattgatcgattattattgct -557

ctttcttgatttgcttctatcagctgcgtaatgaggtgttctaaagatcagctttaattcatttggacaagtgcctcttaataaaacttacctgtactc -457

attttgaaacgatttacgatgataagattgaaagtgaagttaaatttagtctttcaaagttgaaataaaatcttcataaataaaatttaaataatgaa -357

L A F V F K S 401

agattaataaattaacgttcacgtagttaaaaaaataatttaaactctaaacttctaataaaaaatctcaattttccagGACTCGCATTCGTGTTCAAAA -257

I F R L E L N Y T Y P L K Y V L G D S L L G G F H I G A G V N F L 434

GTATTTCCGGCTGGAACCACTACACGTATCCATTGAAATATGTGCTCGGCGATTTCATTGCTCGGTGGATTCCATATTGGAGCTGGTGTCAACTTCTT -157

Gtagagattaattggatgcaagcaccctcaaaaagattttttgaaaaacgataaattcacagaatttcagttcttttctccccctttattgttatt -57

SHP134

ttcatcgtaatgctgtgctagaagtcagagtaaatatgagttttttgtgttctaggaattccatttttcaggaagcaaatttaataaaaattatcgaa 44

SHP164

polyA

tttcttgctctaaagatgttgtacattttatggaaatgttcgtatagtaa

94

SHP135

*hap-1*

SL2  
 M S L R K I N F V T G 11  
 ttcgaacactttatatttctcgttttaaaactgtcgggttttatagtaaactatcttcagaaaaaATGAGCCTACGAAAAATCAATTTCGTAAC TGA 194  
 SHP91 SHP118

N V K K L E E V K A I L K N F E 27  
 AACGTGAAGAAGCTTGAAGAAGTCAAGGCTATTTGAAGAATTCGAGGtaaaatatatttgatattattcgaacgcgaaattttgcgcaaaagtacga 294

tgccgtgtctcaacacgacaatattttgttaaatacaaacgaatgtgcgccttcaaagaaaagtttcaatctttcggtgccgtggagatatttttagagt 394

V S N V D V D L D E F 38  
 tttgtttaaattatatatttgcgtatcgaaaccgggtaccgtaataatcaattaaatattttcagGTTTCAAACGTGGATGTCGATTTGGATGAATT 494  
 SHP165

Q G E P E F I A E R K C R E A V E A V K G P V L 62  
 CCAAGGAGAACCCGAATTTATTGCCGAAAGAAAGTCCCGTGAGGCTGTTGAAGCTGTAAAGGGCCCGTTTGgtatggaaaattgtatttgttctaaaa 594

V E D T S L C F N A M G G L P G P Y I K W F L K N L K P E 91  
 attgtcaaatttcagGTCGAAGACACAAGTTTATGCTTCAACGCAATGGGCGGTCTTCCTGGACCTTATATCAAGTGGTTTTGAAGAATTTGAAACCAG 694  
 SHP129

FIS-18A

*hap-1* continued...

32/32

G L H N M L A G F S D K T A Y A Q C I F 111  
AAGGACTACATAATATGCTAGGtaaatattttaatttttgaaaaaacttatttttcagCCGGATTTTCTGACAAAACCGCCTATGCTCAATGCATCTTT 794

A Y T E G L G K P I H V F A G 126  
GCGTACACTGAAGGACTCGGAAAACCTATTCATGTATTGCTGgtatgattttttgaatttaattctttaattttatatgttaatttagttgtttcattc 894

K C P G Q I V A P R G D T A F G W D P 145  
ctcaatttatgagagattttttttcaatttttctatttcagGAAATGTCTGGTCAAATTGTTGCTCCACGTGGTGATACTGCTTTGGATGGGATCC 994  
SHP130

C F Q P D G F K E T F G E M D K D V K N E I S H R A K A L E L L K 178  
ATGCTTCCAGCCAGATGGTTTTAAAGAAACATTCGGAGAAATGGATAAAGATGTAAAAAATGAAATTTCTCATCGTGCAAAGGCTCTGGAACCTCCTCAAG 1094  
SHP119 SHP120

E Y F Q N N • 184  
GAATATTTTCAGAATAATtaaattattttttctcatctatgcaatttcttgaaaatttgtaagtttccgttggtatgcatttgcttttatttaaaaaa 1194

polyA  
aaagaatatttttacattaatattagatatgagaaaagagtaatttctggattttaaccttcctacaaaagaatatttatatttttgatgatttttta 1294  
SHP93

FIG-10B